IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

In re Patent Application of

FARDEAU et al. Atty. Ref.: 1721-94

Serial No. 10/538,715 TC/A.U.: 1651

Filed: June 10, 2005 Examiner: Kim

For: BACTERIAL STRAINS OF GENUS EXIGUOBACTERIUM, CULTURE METHOD AND USES

* *

October 12, 2010

Mail Stop Appeal Brief - Patents
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

APPEAL BRIEF

Sir:

Applicant hereby appeals the rejection of claim 12, in the Office Action dated January 12, 2010, and submits the present Appeal Brief pursuant to 37 CFR § 41.37.

The application has been twice rejected.

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(1) REAL PARTY IN INTEREST

The real party in interest is INSTITUT DE RECHERCHE POUR LE DEVELOPPEMENT (IRD) , 213, RUE LA FAYETTE, PARIS CEDEX 10, FRANCE F-75480, by way of an Assignment from the appellants, recorded in the U.S. Patent and Trademark Office on June 14, 2006, at Reel 018009, Frame 0634. The address of INSTITUT DE RECHERCHE POUR LE DEVELOPPEMENT (IRD) is now Le Sextant - 44 Bd de Dunkerke, CS 90009, 13572 Marseille FRANCE.

(2) RELATED APPEALS AND INTERFERENCES

The appellant, the appellant's legal representative, and the assignee are not aware of any related prior or pending appeals or interferences or judicial proceedings which will directly affect or be directly affected by or have a bearing on the Board's decision in this appeal.

(3) STATUS OF THE CLAIMS

Claims 8 and 12 are pending.

Independent claim 8 has been allowed.[1]

Independent claim 12 is rejected. The application and the subject matter of independent claim 12 have been twice rejected. Independent claim 12 is the subject of the present appeal.

The application was originally-filed with claims 1-10. Claims 4-6, 9 and 10 were amended, without prejudice, and claim 11 added in an Amendment filed June 14, 2006 and April 5, 2007. Claims 2-7 and 9-11 were canceled, without prejudice, claim 1 amended and claim 12 added in an Amendment filed November 27, 2007. Claims 1, 8 and 12 were further amended in an Amendment After Final Rejection filed May 13, 2008, which was entered upon the filing of the RCE of July 7, 2008. Claim 1 was canceled, without prejudice, and claim 12 amended in an Amendment filed August 14, 2009. Claim 12 was further amended in a Supplemental Amendment filed November 18, 2009 Claims 8 and 12 are pending.

A copy of all the rejected claim 12, i.e., the claim involved in the appeal, is attached as a Claims Appendix, pursuant to Rule 41.37(c)(1)(viii).

[1] See page 1 of the Office Action dated January 12, 2010.

(4) STATUS OF THE AMENDMENTS

A response to the Office Action of January 12, 2010 has not been filed.

(5) SUMMARY OF CLAIMED SUBJECT MATTER

Pursuant to 37 CFR § 41.37(a)(2)(v), the following is a concise explanation of the subject matter defined in each of the independent claims involved in the appeal, which shall refer to the specification by page and line number, and to the drawing, if any, by reference characters.

Independent claim 12 is the only independent claim of the claims on appeal.

The rejected independent claim 12 defines an isolated bacterial strain which is an *Exiguobacterium lactigenes* strain[2], the isolated bacterial strain comprising a 16S rRNA sequence of SEQ ID NO:1[3], the isolated bacterial strain further comprising a DNA sequence, at least 70% of which is capable of hybridizing with genomic or plasmid DNA of the strain deposited on December 5, 2002, under the No. I-2962, with the Collection Nationale de Cultures de Microorganismes (C.N.C.M.)[4], the isolated bacterial strain being thermoresistant, saccharolytic and amylolytic and/or capable of producing L(+) lactate[5], and having growth properties at temperatures of 40 to 50°C, at a pH of 5.4 to 9.15, with an optimum for growth at 45°C, at a pH of approximately 7[6], and a guanine plus cytosine content of its DNA of approximately

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[2] See for example, page 1, lines 4-5 and page 3, lines 30-32 of the specification.
[3] See for example, page 3, lines 11-14, and page 9, lines 10-11 of the specification and originally-filed claim 3.
[4] See for example, page 2, lines 33-39 and page 3, lines 34-38 of the specification, and originally-filed claims 1 and 2.
[5] See for example, page 5, lines 1-5 of the specification and originally-filed claim 4.
[6] See for example, page 8, lines 7-8 and 17-18 and page 10, lines 5-7 of the specification and originally-filed claim 5.

50 mol%[7].

[7] See for example, page 3, liens 21-24 and page 8, lines 30-31 of the specification, and originally-filed claim 6.

(6) GROUNDS OF REJECTION TO BE REVIEWED ON APPEAL

The following ground of rejection are presented for review:

Whether the invention of claim 12 is supported by an adequate written description, as required by 35 U.S.C. § 112, first paragraph.

(7) ARGUMENT

The isolated bacterial strain of independent claim 12 is supported by an adequate written description. One of ordinary skill in the art will appreciate that the applicants were in possession of the claimed invention at the time the application was filed.

The rejection of claim 12 under 35 U.S.C. § 112, first paragraph, should be reversed. Consideration of the following in this regard is requested.

The rejected independent claim 12 defines an isolated bacterial strain which is an *Exiguobacterium lactigenes* strain, the isolated bacterial strain comprising a 16S rRNA sequence of SEQ ID NO:1, the isolated bacterial strain further comprising a DNA sequence, at least 70% of which is capable of hybridizing with genomic or plasmid DNA of the strain deposited on December 5, 2002, under the No. I-2962, with the Collection Nationale de Cultures de Microorganismes (C.N.C.M.), the isolated bacterial strain being thermoresistant, saccharolytic and amylolytic and/or capable of producing L(+) lactate[8], and having growth properties at temperatures of 40 to 50°C, at a pH of 5.4 to 9.15, with an optimum for growth at 45°C, at a pH of approximately 7, and a guanine plus cytosine content of its DNA of approximately 50 mol%. The claimed subject matter is described in the specification and originally-filed claims, as demonstrated above.

As described in MPEP § 2163, there is a

> "strong presumption that an adequate written description of the claimed invention is present when the application is filed. In re Wertheim, 541 F.2d 257, 263, 191 USPQ 90, 97 (CCPA 1976) ("we are of the opinion that the PTO has the initial burden of presenting evidence or reasons why persons skilled in the art would not recognize in the disclosure a description of the invention defined by the claims"). "

As the appealed independent claim 12 is a combination of originally-filed claims 1, 2, 3, 4, 5 and 6 (which depended from claim 1), there is a "strong presumption" that the appealed independent claim 12 is supported by an adequate written description. The Examiner has failed to overcome this "strong presumption" and the Section 112, first paragraph "written description", rejection should be reversed.

The Examiner has asserted that the specification allegedly fails to describe more than the specifically deposited strain which is the subject of allowed independent claim 8.

As explained however in Capon v. Eshhar, 76 USPQ2d 1078, 1084 (Fed. Cir. 2005),

> The "written description" requirement implements the principle that a patent must describe the technology that is sought to be patented; the requirement serves both to satisfy the inventor's obligation to disclose the technologic knowledge upon which the patent is based, and to demonstrate that the patentee was in possession of the invention that is claimed. *See Enzo Biochem*, 296 F.3d at 1330 (the written description requirement "is the quid pro quo of the patent system; the public must receive meaningful

[8] See for example, page 5, lines 1-5 of the specification and originally-filed claim 4.

> disclosure in exchange for being excluded from practicing the invention for a limited period of time"); *Reiffin v. Microsoft Corp.*, 214 F.3d 1342, 1345-46 (Fed. Cir. 2000) (the purpose of the written description requirement "is to ensure that the scope of the right to exclude . . . does not overreach the scope of the inventor's contribution to the field of art as described in the patent specification"); *In re Barker*, 559 F.2d 588, 592 n.4 (C.C.P.A. 1977) (the goal of the written description requirement is "to clearly convey the information that an applicant has invented the subject matter which is claimed"). The written description requirement thus satisfies the policy premises of the law, whereby the inventor's technical/scientific advance is added to the body of knowledge, as consideration for the grant of patent exclusivity.
>
> The descriptive text needed to meet these requirements varies with the nature and scope of the invention at issue, and with the scientific and technologic knowledge already in existence. The law must be applied to each invention that enters the patent process, for each patented advance is novel in relation to the state of the science. Since the law is applied to each invention in view of the state of relevant knowledge, its application will vary with differences in the state of knowledge in the field and differences in the predictability of the science.

Further, the Court of Appeals for the Federal Circuit has explained as follows in In re Kenneth Alonso (2008-1079 Fed. Cir. October 30, 2008) with regard to the written description requirement in the case of a criteria for a claim defining a genus of antibodies.

> The written description requirement of 35 U.S.C. § 112, ¶ 1, is straightforward: "The specification shall contain a written description of the invention … ." To satisfy this requirement, the specification must describe the invention in sufficient detail so "that one skilled in the art can clearly conclude that the inventor invented the claimed invention as of the filing date sought.

> The requirement "serves a teaching function, as a 'quid pro quo' in which the public is given 'meaningful disclosure in exchange for being excluded from practicing the invention for a limited period of time."
>
> The requirement is rigorous, but not exhaustive: "[I]t is unnecessary to spell out every detail of the invention in the specification; only enough must be included to convince a person of skill in the art that the inventor possessed the invention. LizardTech, 424 F.3d at 1345.

The applicants submit that the determination of what is needed to support generic claims to biological subject matter depends on a variety of factors, such as the existing knowledge in the particular field, the extent and content of the prior art, the maturity of the science or technology, the predictability of the aspect at issue, and other considerations appropriate to the subject matter.[9] For example, it is unnecessary for the specification to provide a description of proteins which are already known in the prior art.[10].

The applicants have provided evidence[11] in this regard to demonstrate that the recitation of 70% hybridization of claim 12 is commonly accepted by scientists and those of ordinary skill in the art as a description of related strains. One of ordinary skill in the art will appreciate that this characteristic of the claimed strains along with the additionally recited characteristics of the claimed invention are sufficient to

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[9] See Capon 76 USPQ.2d 1085.
[10] See Capon 76 USPQ.2d 1087.
[11] See Wayne et al "Report of the Ad Hoc Committee on Reconciliation of Approaches to Bacterial Systematics" International Journal of Systematic Bacteriology, Oct. 1987, vol. 37, No. 4, pages 463-464 (copy attached as Evidence Appendix (a))

conclude that the applicants were in possession of the claimed invention at the filing date of the application.

The Examiner acknowledges that Wayne et al demonstrates that strains belonging to the claimed species will be expected to exist, presumably as defined by the criteria confirmed by Wayne et al.[12] The Examiner's rejection appears to be based only on an allegation that the rejected independent claim 12 is too broad.[13] The Examiner appears to believe that further working examples or further strains within the claimed species would be required to demonstrate possession of the claimed invention.

No such further isolated strains or working example however should be required to describe the claimed invention. The Examiner has acknowledged that the applicants have demonstrated and/or that one of ordinary skill will appreciate that further strains will exist within the claimed species, and that such further strains will have the characteristics of and be described by the elements of the rejected claim. The Examiner has failed to indicate or describe or detail what further may be required to describe the claimed invention or to demonstrate that the applicants were in possession of the claimed invention at the time the application was filed.

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[12] "Applicant argued that the percentage of 70% homology or DNA-DNA hybridization or relatedness would be acceptable in the art, referring Wayne et al. It is understood that the percentage cited by Wayne et al. is a criteria for a phylogenetic definition of species, and it is understood that certainly there are strains belong to the same species of Exiguobacterium lactigenes. Considering the broadest scope of the instant claim and a single species (strain) disclosed in the specification (e.g. I-2962), it is not considered that the specification provides the written description that the inventors possess entire strains of a species of Exiguobacterium lactigenes as claimed." See page 5 of the Office Action dated January 12, 2010 (emphasis added).

In Enzo Biochem v. Gen-Probe, Inc., 63 USPQ2d 1609, 1613 (Fed. Cir. 2002), the court stated that the written description requirement would be met for all of the claims of the patent at issue if the functional characteristic of the claimed invention was coupled with a disclosed correlation between that function and a structure that is sufficiently known or disclosed. The structure of the claimed invention, such as is described by the 70% hybridization requirement, will be appreciated by one of ordinary skill to be related to the additionally recited functional characteristics of the claimed strains, as evidenced by, for example, Wayne et al

Finally, the applicants note that the Federal Circuit has stated that as long as an applicant has disclosed a "fully characterized antigen," either by its structure, formula, chemical name, or physical properties, or by depositing the protein in a public depository, the applicant can then claim an antibody by its binding affinity to that described antigen.[14]

In the present application, the strains of the rejected claim are characterized by their relationship to the fully characterized and deposited strain recited in the claim.

As explained by the Federal Circuit in In re Kenneth Alonso[15]

> A genus can be described by disclosing: (1) a representative number of species in that genus; or (2) its "relevant identifying characteristics," such as "complete or partial structure, other physical and/or chemical properties, functional characteristics

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[13] Id.
[14] See Noelle v. Lederman, 69 USPQ2d 1508, 1514 (Fed. Cir. 2004).
[15] 88 USPQ2d 1849, 1852 (Fed. Cir. 2008).

> when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics."

In the present specification, the applicants have described and deposited a representative species, described representative sequence of the 16s rRNA required by the claimed strains and described a combination of physical and chemical properties as well as functional characteristics of the claimed strains. One of ordinary skill will appreciate that the applicants were in possession of the claimed invention at the time the application was filed.

The written description requirement is satisfied by the applicants conveyance with reasonable clarity to those skilled in the art that as of the filing date the applicants were in possession of the claimed invention.[16] An applicant shows possession of the claimed invention by describing the claimed invention with all of its limitations using such descriptive means as words, structures, figures, diagrams, and formulas that fully set forth the claimed invention.[17] Possession may be shown in a variety of ways including description of an actual reduction to practice, or by showing that the invention was "ready for patenting" such as by the disclosure of drawings or structural chemical formulas that show that the invention was complete, or by describing distinguishing identifying characteristics sufficient to show that the

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[16] See Ralston Purina Co. v. Far-Mar-Co., Inc., 227 USPQ 177, 179 (Fed. Cir. 1985) (quoting In re Kaslow, 217 USPQ 1089, 1096 (Fed. Cir. 1983)).
[17] See Lockwood v. American Airlines, Inc., 41 USPQ2d 1961, 1966 (Fed. Cir. 1997).

applicant was in possession of the claimed invention.[18] The applicants are not required to show a reduction to practice or exemplification of every aspect of the claimed invention to demonstrate an adequate written description, as appears to be required by the present Examiner.

The claims are supported by an adequate written description. Basis for the rejected claim is found throughout the specification and originally-filed claims such that there is a strong presumption that an adequate written description of the claimed invention was present in the specification as filed. The Examiner has failed to rebut this presumption. The specification is not required to exemplify or reduce to practice every aspect or embodiment of the claimed invention. One of ordinary skill in the art will appreciate that the applicants were in possession of the claimed invention at the time the application was filed.

Reversal of the Section 112, first paragraph "written decryption", rejection of claim 12 is requested.

The pending claims are submitted to be in condition for allowance and Reversal of the final rejection is requested.

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[18] See, for example, Pfaff v. Wells Elecs., Inc., 525 U.S. 55, 68, 119 S.Ct. 304, 312, 48 USPQ2d 1641, 1647 (1998); Regents of the University of California v. Eli Lilly, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997); Amgen, Inc. v. Chugai Pharmaceutical, 18 USPQ2d 1016, 1021 (Fed. Cir. 1991) (one must define a compound by "whatever characteristics sufficiently distinguish it").

Respectfully submitted,

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(8) CLAIMS APPENDIX

12. An isolated bacterial strain which is an *Exiguobacterium lactigenes* strain

said isolated bacterial strain comprising a 16S rRNA sequence of SEQ ID NO:1,

said isolated bacterial strain further comprising a DNA sequence, at least 70% of which is capable of hybridizing with genomic or plasmid DNA of the strain deposited on December 5, 2002, under the No. I-2962, with the Collection Nationale de Cultures de Microorganismes (C.N.C.M.),

said isolated bacterial strain being thermoresistant, saccharolytic and amylolytic and/or capable of producing L(+) lactate, and

having growth properties at temperatures of 40 to 50°C, at a pH of 5.4 to 9.15, with an optimum for growth at 45°C, at a pH of approximately 7, and

a guanine plus cytosine content of its DNA of approximately 50 mol%.

(9) EVIDENCE APPENDIX

Attached:

(a) Wayne et al "Report of the Ad Hoc Committee on Reconciliation of Approaches to Bacterial Systematics" International Journal of Systematic Bacteriology, Oct. 1987, vol. 37, No. 4, pages 463-464 (of record and considered by the Examiner as evidenced by the initialed PTO 1449 Form indexed at January 12, 2010 in the PTO IFW).

(10) RELATED PROCEEDINGS APPENDIX

Attached:

NONE

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INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY, Oct. 1987, p. 463–464 Vol. 37, No. 4
0020-7713/87/040463-02$02.00/0

Report of the Ad Hoc Committee on Reconciliation of Approaches to Bacterial Systematics

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Veterans Administration Medical Center, Long Beach, California[1]; Centers for Disease Control, Atlanta, Georgia[2]; University of Maryland, College Park, Maryland[3]; Institut Pasteur, Paris, France[4]; University of Munich, Munich, Federal Republic of Germany[5]; National Institute of Dental Research, Bethesda, Maryland[6]; Virginia Polytechnic Institute and State University, Blacksburg, Virginia[7]; University of Western Ontario, London, Ontario, Canada[8]; University of Kiel, Federal Republic of Germany[9]; University of California, Davis, California[10]; University of Bonn, Bonn, Federal Republic of Germany[11]

Bacterial taxonomy, which began as a largely intuitive process, has become increasingly objective with the advent of numerical taxonomy and techniques for the measurement of evolutionary divergence in the structure of semantides, i.e., large, information-bearing molecules such as nucleic acids and proteins. These developments have forced the adoption of changes in nomenclature, sometimes with disruptive or even perilous consequences (2). Since the present nomenclatural system evolved during a period when hierarchial taxonomic divisions were only vaguely defined, it has become important to reexamine that system in the light of newer taxonomic understanding. Accordingly, an ad hoc committee of the International Committee for Systematic Bacteriology was convened for a Workshop on Reconciliation of Approaches to Bacterial Systematics at the Institut Pasteur, Paris, on 14 to 16 May 1987.

Perspectives. To arrive at a common ground of understanding, the committee reviewed the current state of bacterial systematics from the following perspectives:

(i) Phylogenetic. Phylogenetic studies are directed at a basic understanding of pathways through which taxa have evolved from primordial and recent ancestors, calculated from analyses of evolutionary distances between selected semantides.

(ii) Descriptive. Descriptive research represents the bridge between semantide-based phylogenetic taxonomy and traditional phenotype-based bacterial systematics. Organisms are described in phenotypic terms, and the descriptions help define a taxonomic group that may also be recognized at the phylogenetic level.

(iii) Diagnostic. Diagnosis involves the selection of features from those in a phenotypic description, or of probes derived from phylogenetic analyses, in a way that permits the recognition of an unknown strain and the assignment of a label to it. The most useful labels for applied purposes are names at the genus, species, and subspecies levels; infrasubspecific categories that are not governed by the Bacteriological Code (1) may be useful for recognition of special attributes.

(iv) Associative. Associative studies use a name to evoke practical information about a strain, such as its medical, industrial, or ecologic significance.

The committee offers the following conclusions and recommendations.

HIERARCHICAL TAXONOMY

An ideal taxonomy would involve one system. A single formal overall system appears to be adequate, and a second system is not needed if vernacular grouping is retained for diagnostic purposes.

There was general agreement that the complete deoxyribonucleic acid (DNA) sequence would be the reference standard to determine phylogeny and that phylogeny should determine taxonomy. Furthermore, nomenclature should agree with (and reflect) genomic information.

The group agreed that hierarchical consistency is essential but recognized that the depth in a ribonucleic acid (RNA) dendrogram at which a given hierarchical line is to be drawn may vary along different major branches of the dendrogram and will be strongly influenced by phenotypic consistency at each level. This is a consequence of differences in ages of the different branches and the recognition that older branches will exhibit greater nucleic acid structural genetic drift, even as environmental constraints tend to limit phenotypic drift.

A cautionary note about hierarchical interpretation was expressed with the recommendation that active searches continue for additional powerful semantides independent of the ribosomal RNA cistrons.

The chemotaxonomic approach has two sets of derivative data: structural phenetic (including "signatures") and phylogenetic (evolutionary). There should not be further designation of hierarchical levels without substantial chemotaxonomic and sequence data to support the proposal.

Species, subspecies, and infrasubspecific categories. At present, the species is the only taxonomic unit that can be defined in phylogenetic terms. In practice, DNA reassociation approaches the sequence standard and represents the best applicable procedure at the present time. *The phylogenetic definition of a species generally would include strains with approximately 70% or greater DNA-DNA relatedness and with 5°C or less ΔT_m. Both values must be considered.* Phenotypic characteristics should agree with this definition and would be allowed to override the phylogenetic concept of species only in a few exceptional cases.

It is recommended that a distinct genospecies that cannot be differentiated from another genospecies on the basis of any known phenotypic property not be named until they can be differentiated by some phenotypic property.

Subspecies designations can be used for genetically close organisms that diverge in phenotype. There is some evi-

* Comments on the conclusions and recommendations included in this report are welcome and should be sent to Lawrence G. Wayne, Tuberculosis Research Laboratory(151), Veterans Administration Medical Center, 5901 East Seventh St., Long Beach, CA 90822.

dence, based on frequency distribution of ΔT_m values in DNA hybridization, that the subspecies concept is phylogenetically valid and can be distinguished from the infrasubspecific variety concept, which is based solely on selected "utility" attributes, but not demonstrable by DNA reassociation. *There is a need for further guidelines for designation of subspecies.*

Genera. Genera form the essential basis of bacterial systematics, and each genus must remain subject to continuing assessment. A degree of flexibility in circumscription is necessary. Unfortunately, there is currently no satisfactory phylogenetic definition of a genus. *The scope of the definition may differ among genera*, as for any other higher taxa.

Families. Families can be retained as long as they are consistent in terms of chemotaxonomic and hybridization or sequence data. Any other hierarchical level established between family and division must also be consistent in terms of supporting taxonomic data.

Divisions. It is clear that there are at least 15 clearly separated lineages of great antiquity in evolutionary terms at the level of division or greater.

Kingdom. There is no need at this time for more than one kingdom, but there may be need for a term to describe major primary lineages. A rank such as phylum may be needed in the future.

NOMENCLATURE

After a review of alternative approaches to the occasional conflict between binomials based on strict phylogenetic relationships at the species level and the practical application of the binomials, the following recommendations were made.

Nomenclature should reflect genomic relationships to the greatest extent possible. Rare exceptions are sanctioned under the emendation to Rule 56a embodied in Minute 7i of the Judicial Commission (Int. J. Syst. Bacteriol. 37:85–87, 1987), introducing the concept of a "nomen periculosum." It is anticipated that this concept need be applied in only a limited number of cases and hoped that this type of problem will disappear as new taxonomic methods and interpretations are more universally applied. *A mechanism is needed for broad dissemination of information about those cases where such nomenclatural discrepancies have been sanctioned.*

As needed, various vernacular appendices that pertain to needs for special purposes (medical, veterinary, agriculture, industry, etc.) including information about traits coded by plasmids, phages, and other extrachromosomal agents should be applied. These infrasubspecific "utility" categories are not governed by the Bacteriological Code. In certain medical situations, identification of the presence of certain virulence factors may be more important than the species name.

Regarding inadequate nomenclature, it is recommended that formal nomenclature is needed for the major divisional groupings. "Gram positives" should be Firmicutes as presently defined. The term "purple bacteria" causes confusion because it includes more than phototrophic bacteria, which is good reason for a formal name to be established.

OTHER CONCERNS

Special difficulties are expected in accomplishing the taxonomic reorganization of the major phylogenetic taxon listed as "the purple photosynthetic bacteria and their relatives" (3), and this includes most of the classically defined gram-negative genera, both photosynthetic and chemosynthetic, in the alpha, beta, gamma, and delta groups of the purple bacteria. Thus, the major task of the greatest practical importance is the development of a taxonomic and nomenclatural approach to resolving the linked phylogenetic lineages of the remarkably diverse metabolic types of organisms within each of the groupings. Urgency is dictated by the large number of bacteria involved and by the many species that are crucial in ecological and diagnostic bacteriology. A number of genera must be reassessed, although many will persist in part, if not as a whole. There are gaps in our knowledge because the molecular/genetic surveys are incomplete. The first task is the definition and phylogenetic circumscription of the genera in this phylogenetic taxon, with inclusion of type strains of species in the genera. *It is recommended that this problem be assigned for special study by an ad hoc subcommittee of the International Committee on Systematic Bacteriology.*

Research should be directed toward solving the growth and diagnostic problems of noncultivable or hardly cultivable organisms, e.g., cholera somnicells, nongerminable endospores, and organisms not cultivable axenically but cultivable in multiorganism systems, such as representatives of consortia, *Pasteuria*, *Planctomyces*, etc. The Code may have to be emended to clarify the status of multiorganism cultures as type material; e.g., see Rule 18a and Advisory Note C, Chapter 4 (1).

A whole base line of bacterial taxonomy of various ecosystems is urgently needed, as is a broader knowledge of species distribution in ecosystems and improved knowledge of little known bacteria. ("Less than 20% of the bacteria are known.") Encouragement must be given to systematic studies and the search for new chemotaxonomic markers. Recognition of the importance of effective taxonomic understanding to all fields, basic and applied, and especially to biotechnology has been slow to develop, although the need is great. The group recognized, also, that ecologically relevant characterization of the members of complex bacterial populations requires the identification of these characters in a burgeoning field of biochemical/molecular/genetic research.

An overall concern of members of the Committee was that any phylogenetically based taxonomic schemes that result must also show phenotypic consistency.

ACKNOWLEDGMENTS

The International Committee on Systematic Bacteriology and the members of the Ad Hoc committee are grateful to the Bacteriology Division of the International Union of Microbiological Societies, to the International Council of Scientific Unions, and to the Bergey's Manual Board of Trustees for the provision of funds supporting the meeting, and to the Institut Pasteur (Paris) for its hospitality.

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